

Systematic Review

Detection of Human Papillomavirus in Laryngeal Squamous Cell Carcinoma: Systematic Review and Meta-analysis

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Background: Recent studies have reported a human papillomavirus (HPV) prevalence of 20% to 30% in laryngeal squamous cell carcinoma (LSCC), although clinical data on HPV involvement remain largely inconsistent, ascribed by some to differences in HPV detection methods or in geographic origin of the studies.

Objective: To perform a systematic review and formal meta-analysis of the literature reporting on HPV detection in LSCC.

Methods: Literature was searched from January 1964 until March 2015. The effect size was calculated as event rates (95% confidence interval [CI]), with homogeneity testing using Cochran's Q and I^2 statistics. Meta-regression was used to test the impact of study-level covariates (HPV detection method, geographic origin) on effect size. Potential publication bias was estimated using funnel plot symmetry.

Results: One hundred seventy nine studies were eligible, comprising a sample size of 7,347 LSCCs from different geographic regions. Altogether, 1,830 (25%) cases tested HPV-positive considering all methods, with effect size of 0.269 (95% CI: 0.242 to 0.297; random-effects model). In meta-analysis stratified by the 1) HPV detection technique and 2) geographic study origin, the between-study heterogeneity was significant only for geographic origin ($P = .0001$). In meta-regression, the HPV detection method ($P = .876$) or geographic origin ($P = .234$) were not significant study-level covariates. Some evidence for publication bias was found only for studies from North America and those using non-polymerase chain reaction methods, with a marginal effect on adjusted point estimates for both.

Conclusions: Variability in HPV detection rates in LSCC is explained by geographic origin of study but not by HPV detection method. However, they were not significant study-level covariates in formal meta-regression.

Key Words: Laryngeal cancer, papillomavirus, meta-analysis, meta-regression, study heterogeneity, publication bias, detection method, geographic region.

Level of Evidence: NA

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Additional Supporting Information may be found in the online version of this article.

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INTRODUCTION

The causal relationship between high-risk human papillomavirus (HPV) infection and head and neck squamous cell carcinoma (HNSCC) is well established, following the reports of Syrjänen and coworkers, who first suggested this association more than 3 decades ago.¹ Since then, several epidemiologic and biological studies have implicated HPV infection, mainly the HPV 16 genotype, as a potential etiological factor for the development of tumors in the upper aerodigestive tract, especially in the oropharynx.^{2–6} Conversely, the role of high-risk HPV infection in nonoropharyngeal HNSCC is still under discussion, despite an ever-increasing volume of studies and meta-analyses published during the past decades.

The majority of HPV-related squamous cell carcinomas (SCC) arise in the oropharynx (i.e., tonsils and base of the tongue), where the reticulated lymphoepithelium is susceptible to HPV infection-associated oncogenesis.⁷ Current literature reports an HPV prevalence greater than 50% in tonsillar carcinomas,² and recent studies,

particularly those in the United States, show that up to 80% of oropharyngeal SCCs are HPV related.⁸ However, only some 40% of these tumors are transcriptionally active with HPV 16 E6 and E7 expression.⁸ Conversely, even though high-risk HPV can be found in a minority of SCCs from nonoropharyngeal sites (e.g., oral cavity, hypopharynx, nasopharynx, and larynx), using a rigorous definition, the truly transcriptionally active HPV rates are generally low for oral cavity and larynx cancer—16.3% and 8.6%, respectively.⁹

Laryngeal squamous cell carcinoma (LSCC) represents the second most common malignancy of the head and neck worldwide,^{10,11} with 151,000 incidence cases diagnosed worldwide in 2008.¹² Traditionally, LSCC is ascribed to tobacco and alcohol exposure. However, molecular evidence has linked HPV, particularly HPV-16, in the pathogenesis of LSCC.⁶ Recent meta-analyses have reported HPV prevalence of 20% to 30% for LSCC.^{5,13–15} However, the mere presence of HPV DNA in a tumor does not necessarily indicate that the virus is driving or contributing to tumor development or progression.¹⁶ Methods detecting transcriptionally active HPV, including CDKN2A (p16) immunohistochemistry, quantitative polymerase chain reaction (PCR) or in situ hybridization for HPV DNA or E6/E7 mRNA, might be necessary to demonstrate a biologically active virus.^{16–18}

The HPV detection rate among LSCC samples has remained highly variable, ranging from 0% to 85%.^{14,19} Some authors have reported that HPV prevalence in LSCC can vary geographically and by ethnic group.^{3,6,14,20–22} possibly due to genetic diversity or environmental and cultural differences.²⁰ Besides geographic and ethnic differences, the disparity in HPV prevalence usually seen among studies is due to an inadequate distinction of patients with LSCC from those with other cancers of the head and neck region, such as oropharyngeal SCC.⁴ Additionally, differences in sensitivity and specificity of HPV genotyping methods and diagnostic criteria,^{3,23} in addition to the limited spectrum of HPV types analyzed, as well as differences among HPV, have contributed to the inconsistent results regarding the HPV prevalence rate in LSCC.

Herein, a systematic review and formal meta-analysis was performed on HPV prevalence in LSCC, covering all reports published until March 2015, without any restrictions concerning the HPV detection method and geographic origin of the study. The main objective was to estimate the overall HPV prevalence in LSCC and to identify whether inconsistent results among studies are due to different geographic locations and/or HPV detection methods.

MATERIALS AND METHODS

Data Abstraction

We identified eligible studies by searching MEDLINE and reference lists from original articles, book chapters, and reviews from January 1964 until March 2015. No language limitations were imposed. The search terms included: papillomavirus, HPV, larynx, squamous cell, verrucous carcinoma, basaloid squamous cell, papillary squamous cell, cancer, carcinoma, head and neck

cancer. All publications that appeared in peer-reviewed journals were eligible, irrespective of HPV detection method. Furthermore, the identified reports had to include exact numbers of analyzed cases and those testing HPV-positive.

Altogether, 783 abstracts were derived from the database, covering the years 1964 through 2015. This abstract list was cross-checked against the other databases (Embase and Cochrane) to find out whether any potential studies were missed in MEDLINE. No such case was identified; however, many of the studies detected in MEDLINE were missing in these two databases. Thus, the final selection was based on these 783 abstracts.

For the present meta-analysis, a total of 179 original studies were determined eligible, fulfilling the above-defined criteria. The vast majority of the ineligible studies surveyed were case reports, case series, or clinical and/or epidemiological studies (including treatment reports), without HPV testing, or were studies on HPV in laryngeal papillomas. The formal meta-analysis was focused on LSCC only, where the different histological types: 1) SSC, 2) basaloid squamous cell carcinoma, 3) verrucous carcinoma, 4) spindle squamous cell carcinoma, and 5) papillary squamous cell carcinoma were treated as subgroups within the study. In final analyses, all subtypes were combined, because all represent LSCC variants.

From the summaries and/or body texts of each eligible study, we extracted the following data: histological types of cancer, HPV detection methods, geographic region of the study, total number of cases analyzed, HPV genotypes analyzed and/or detected, number testing HPV-positive, percent of HPV positivity, authors, and publication year (see Supporting Table 1 in the online version of this article). This list of items represents a modification of the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) statements,²⁴ adopted specifically for this purpose, where event rates represent the effect size recorded for each original study.

The authors divided HPV detection methods into two categories: PCR and non-PCR methods. The non-PCR methods comprises the following methods: immunohistochemistry (IHC), Southern blot hybridization (SB), dot blot hybridization (DB), filter in situ hybridization (FISH), hybrid capture II (HCII), in situ hybridization (ISH), non-isotopic in situ hybridization (NISH), and chromogene in situ hybridization (CISH). When more than one detection method was used, that particular study was categorized into the PCR group whenever PCR was included. In this case, only the PCR results were used in calculations. According to their geographic location, the studies were divided into the following groups: North America, Central and South America, Europe, China, other Asia, and Pacific, Africa/Middle East, and international (data from several regions).

Statistical Analyses

A specific software Comprehensive Meta Analysis (version 2.2.064; Biostat Inc., Englewood, NJ), was used to perform the meta-analysis. The software calculates the event rates based on the events and sample size data. To assess overall heterogeneity in event rates between the different studies, Cochran's *Q* homogeneity *P* value as well as *I*² statistics (for percentage of variation) were used.²⁵ To explore the eventual publication bias, funnel plots were drawn by plotting the logit event rates by their precision (1/SE),²⁶ evaluated for asymmetry using the following statistics: 1) Begg and Mazumdar rank correlation,²⁷ 2) Egger's test of the intercept (regression),²⁸ and 3) Duval and Tweedie's "trim and fill" method,²⁹ which imputes the results that are hypothetically missing due to publication bias.

TABLE I.
Meta-analysis of the 179 Studies on Laryngeal Squamous Cell Carcinoma Stratified by the Human Papillomavirus Detection Method.

HPV Detection Method	No. of Studies	Events	Sample Size	Point Estimates of Event Rates (Fixed-Effects Model)		Point Estimates of Event Rates (Random-Effects Model)		Homogeneity (Cochran's Q)*	I^2 *	Homogeneity (P Value)*
				Point Estimate	95% CI	Point Estimate	95% CI			
PCR	127	1,387	5,161	0.311	0.297 to 0.325	0.271	0.241 to 0.302	564.857	77.693	.0001
Non-PCR	52	443	2,186	0.243	0.223 to 0.265	0.271	0.215 to 0.335	256.771	79.748	.0001
Summary	179	1,830	7,347	0.292	0.281 to 0.304	0.269	0.242 to 0.297	846.783	78.861	.0001
Total within (FE)								821.628		.0001
Total between (FE)								25.155		.0001
Total between (RE)								0.0000		.985

*Only calculated for fixed-effects model.

CI = confidence interval; FE = fixed-effects model; PCR = polymerase chain reaction; RE = random-effects model.

To assess the variation in event rates due to the differences between individual studies, we evaluated the study characteristics using stratified meta-analyses and restricted maximum likelihood meta-regression. Meta-regression formally compares these differences in event rates across the selected study-level covariates and estimates the among-study variance.³⁰ Because of inherent differences in sensitivity between the different HPV detection methods (PCR and non-PCR), meta-analyses were performed across these strata. Similarly, to distinguish true study-specific effects from random variation, all analyses were also stratified by the geographic regions of their origin, another potential source for variability in HPV prevalence. These two study characteristics (detection method and geographic location) were also tested as study-level covariates in meta-regression.

Sensitivity analysis was performed to assess the influence of each individual study on the strength and stability of the meta-analytic results, using the one-by-one study removal and evaluated by descriptively comparing the magnitude and precision of the random-effects summary event rates.

RESULTS

Eligible Studies

A total of 179 studies (see Supporting Table 1 in the online version of this article) were considered eligible for the present analysis,^{3,4,9,16,19,31–204} comprising a sample size of 7,347 LSCCs with 1,830 events (approximately 25% of HPV positivity for all methods). In addition, some studies on HPV prevalence in recurrent respiratory papillomatosis (RRP), juvenile-onset papillomas, and adult-onset papillomas were included as far as they included also LSCC cases (metachronous or derived from RRP). A total of 5,161 samples were analyzed with PCR including 1,387 events (26.8% HPV positivity), whereas 2,186 samples were examined by non-PCR methods, with 443 events (20.3% HPV positivity) (Table I). The methods used to evaluate the HPV involvement include the following: PCR and non-PCR methods (IHC, DB, SB, ISH, FISH, NISH, HCII, and CISH). In studies using more than one technique, PCR results were computed whenever available^{3,4,16,19,42,46,48,51,52,54,56–59,61,62,64–69,72,74–77,79,81–87,91,92,94–98,100,101,103–106,108–111,113–136,138–144,146–149,151–153,156–163,166–173,175–184,185,187,190,191,195–197,200–202} Conversely, when PCR was not used or its results were not available, the study was included in the non-PCR

method group.^{9,31–41,43–45,47,49,50,53,55,60,63,70,71,73,78,80,88–90,93,99,102,107,112,137,145,150,154,155,164,165,174,185,188,189,192–194,198,199,203,204}

Analytical Results

Point estimates of event rates. The crude HPV-positivity (1,830/7,347) translates to event rates of 0.292 (95% confidence interval [CI] 0.281 to 0.304) using the fixed-effects (FE) model, and 0.269 (95% CI: 0.242 to 0.297) using the random-effects (RE) model. There is a significant heterogeneity between the studies using PCR and non-PCR techniques (Cochran's Q statistics, $P = .0001$) (Table I). This also applies to overall comparison within strata ($P = .0001$), but not for between strata ($P = .985$). The percentage of variation (I^2) is highest (79.7%) for non-PCR-based studies. Using the RE model, both PCR and non-PCR techniques give exactly the same point estimates of HPV prevalence (0.271, 27.1%).

There is significant heterogeneity between the studies from different regions ($P = .0001$), with a variation of 68.9% (North America) to 78% (Europe) (Table II). The highest effect size (39.9%) is found in studies derived from China, followed by those conducted in Central and South America (29%) and Europe (27.9%). The between-strata comparison (RE model) indicates that the heterogeneity between the studies from different geographic regions is statistically significant ($P = .0001$).

Meta-regression. In meta-regression for HPV methods, the PCR method ($n = 127$) resulted in a point estimate that was significantly different ($P = .0001$) from the non-PCR methods ($n = 52$, reference), even though the HPV detection method was not a significant study-level covariate ($P = .876$) in meta-regression (Table III).

In meta-regression for geographic location, all locations except Europe ($P = .023$) resulted in point estimates that were significantly different from the reference (North America). However, in meta-regression, the geographic origin of the study did not have a significant impact on the effect size ($P = .234$) (Table IV).

TABLE II.
Meta-analysis of the 179 Studies on Laryngeal Squamous Cell Carcinoma Stratified by Their Geographic Area.

HPV Detection Method	No. of Studies	Events	Sample Size	Point Estimates of Event Rates (Fixed-Effects Model)		Point Estimates of Event Rates (Random-Effects Model)		Homogeneity (Cochran's Q)*	I ² *	Homogeneity (P Value)*
				Point Estimate	95% CI	Point Estimate	95% CI			
North America	45	370	1,652	0.236	0.214 to 0.259	0.246	0.201 to 0.298	141.779	68.966	.0001
Central and South America	14	190	640	0.324	0.286 to 0.364	0.290	0.217 to 0.377	57.424	77.361	.0001
Europe	82	828	3,266	0.308	0.290 to 0.327	0.279	0.238 to 0.323	371.602	78.202	.0001
Other Asia and Pacific	19	131	931	0.178	0.152 to 0.209	0.168	0.116 to 0.237	71.601	74.861	.0001
China	17	307	770	0.415	0.378 to 0.452	0.399	0.323 to 0.479	68.830	75.301	.0001
Africa and ME [†]	1	1	10							
Intercontinental [†]	1	3	78							
Summary	179	1,830	7,347	0.292	0.281 to 0.304	0.269	0.242 to 0.297	846.783	78.861	.0001
Total within (FE)								711.236		.0001
Total between (FE)								135.547		.0001
Total between (RE)								25.2057		.0001

*Only calculated for fixed-effects model.

[†]Only one study, meta-analysis redundant (omitted from the summary effect analysis).

CI = confidence interval; FE = fixed effects; RE = random effects.

Publication bias. There was no evidence for publication bias among studies based on PCR. For studies using non-PCR techniques, there was some evidence of publication bias. Duval and Tweedie's trim-and-fill method imputed three hypothetically missing studies, with a seemingly sizeable effect on adjusted point estimates (from 0.201 to 0.316), but this difference was not statistically significant as tested by Begg ($P = .138$) and Egger's ($P = .114$) tests.

There was no evidence of publication bias among studies from Central and South America, China, other Asia and Pacific, and from Europe. For studies from North America, the Duval and Tweedie's trim-and-fill method imputed two hypothetically missing studies, with a slight effect on adjusted point estimates (from 0.191 to 0.289), which was not statistically significant: Begg ($P = .071$) and Egger's ($P = .134$).

Sensitivity analysis. Meta-analytic results seemed robust to all ($n = 179$) one-by-one study removals, with no change in the magnitude and precision of the FE and RE summary point estimates of the effect size.

DISCUSSION

This meta-analysis with formal meta-analysis and meta-regression was performed to assess whether the wide variation in HPV prevalence in LSCC is due to different detection techniques as reported earlier.^{3,5,15,23} There is little doubt that a marked heterogeneity exists between the studies based on PCR and non-PCR methods using the Q test and I^2 index (Table I). This marked heterogeneity justifies the adoption of the RE model to analyze the summary statistics.^{25,205–209} Using the RE model, the most important conclusion implicates that there is no true heterogeneity between studies using different HPV detection techniques, as indicated by the nonsignificant homogeneity P value ($P = .985$) for the between-study comparison. Thus, we can revisit the concept raised in several studies suggesting that the differences in HPV prevalence in LSCC would be explained by different HPV detection techniques (intermethod variations)⁵ or due to differences in detection criteria in the same method (intramethod variations).^{47,210,211}

TABLE III.
Effect of HPV Detection Method on the Effect Size in Maximum Likelihood Meta-regression.

Study-Level Covariates	No. of Studies (Homogeneity P Value)*	Effect Size [†]		Difference in Effect Size Estimates [‡]		
		Point Estimate	95% CI	Difference in Point Estimates	95% CI	P Value
Non-PCR	52 (.0001)	0.271	0.215 to 0.335	1.000		Ref
PCR	127 (.0001)	0.271	0.241 to 0.302	0.065	0.044 to 0.086	.0001
Meta-regression for both methods	Slope: 0.028 (95% CI: -0.323 to 0.379) ($P = .876$); intercept: -1.044 (95% CI: -1.510 to -0.578) ($P < .001$)					

Slope: effect parameter (= regression coefficient β_1); intercept (= coefficient β_0).

*Cochran's Q.

[†]Random-effects model.

[‡]Calculated using Stata.

CI = confidence interval; HPV = human papillomavirus; PCR = polymerase chain reaction.

TABLE IV.
Effect of Geographic Origin of the Study on the Effect Size in Maximum Likelihood Meta-regression.

Study-Level Covariates, Geographic Origin of Study	No. of Studies (Homogeneity <i>P</i> Value)*	Effect Size†		Difference in Effect Size Estimates‡		
		Point Estimate	95% CI	Difference in Point Estimates	95% CI	<i>P</i> Value
North America	45 (.0001)	0.246	0.201 to 0.298	1.000		Ref
Central and South America	14 (.0001)	0.290	0.217 to 0.377	0.072	0.032 to 0.113	.0001
Europe	82 (.0001)	0.279	0.238 to 0.323	0.029	0.004 to 0.054	.023
Other Asia and Pacific	19 (.0001)	0.168	0.116 to 0.237	−0.083	−0.113 to −0.053	.0001
China	17 (.0001)	0.399	0.323 to 0.479	0.175	0.135 to 0.215	.0001
Africa/ME§			1			
Intercontinental§			1			
Meta-regression for all	Slope: 0.072 (95% CI: −0.046 to 0.191) (<i>P</i> = .234); intercept: −1.191 (95% CI: −1.555 to −0.827) (<i>P</i> < .001)					

Slope: effect parameter (= regression coefficient β_1), intercept (= coefficient β_0)

*Cochran's *Q*.

†Random-effects model.

‡Calculated using Stata.

§Studies omitted from calculations.

CI = confidence interval.

The other study-level covariate was the geographic origin of the study, also listed as a potential cause of variation in HPV prevalence.^{6,15,23} To validate this concept, we performed a meta-analysis stratified by the geographic area covered by the study (Table II). Both the *Q* test and the *I*² index demonstrated a marked heterogeneity between the studies within all different geographic areas, irrespective the number of studies included in each stratum. Both the within-strata and between-strata comparisons were significant, confirming the substantial heterogeneity between 1) the studies analyzing LSCC in the same geographic area and between 2) the studies assessing LSCC from different geographic areas. In addition, when the RE model was used to interpret the summary statistics, a significant (*P* = .0001) homogeneity *P* value was obtained for the between-strata comparison. This implicated that this wide variation (16.8% to 39.9%) in HPV prevalence from different geographic regions is significant according to the strict meta-analytical criteria. Table II depicts that the extreme of variation occurred in geographic areas with intermediate number of studies, whereas the summary effect size is within a rather narrow range (24.6%–27.9%) in regions with larger number of studies such as Europe and North America, emphasizing the need for meta-regression.

We also performed meta-regression to formally compare these differences in summary effect sizes.²⁹ In meta-regression with the HPV detection method as the covariate, the regression coefficient for the effect parameter (β_1 , or slope) was not statistically significant (*P* = .876) (Table III). The same was true when the geographic area of the study (*P* = .234) (Table IV), was tested for its impact as a study-level covariate. These data formally confirmed that HPV detection method and geographic area of the study are not significant study-level covariates accounting for the heterogeneity of the summary effect size estimates in LSCC studies.

Some evidence for publication bias was detected, but this usually had an insignificant effect on the

adjusted point estimates in the stratified meta-analysis. Most importantly, there was no evidence on publication bias among PCR-based studies, and the slight publication bias among the non-PCR-based studies resulted in an insignificant change (Begg test, *P* = .138; Egger test, *P* = .114) of the point estimates (20.1%–31.6%). As to the geographic areas, some publication bias was evident only for studies from North America, with a slight impact on summary point estimates (19.1%–28.9%), which also proved to be nonsignificant (Begg test, *P* = .071; Egger test, *P* = .134).

One of the potential limitations of the present meta-analysis is associated with the shortcomings of the *Q* statistic, known to have a poor power to detect true heterogeneity in meta-analysis including a small number of studies, but excessive power to detect even insignificant variability when a large number of studies is available.^{25,205–209} This can be a potential weakness only when the meta-analysis is stratified by HPV detection method and geographic areas of the study, which inevitably leads to strata with limited number of studies. This, however, is compensated by the *I*² index, because the indices obtained from meta-analyses with different numbers of studies and different effect metrics are directly comparable.²⁰⁹

Taken together, this meta-analysis based on 179 eligible studies on HPV detection in LSCC implicates that HPV prevalence in LSCC was 25%, and it varies according to 1) HPV detection method and 2) geographic origin. However, in stratified meta-analysis, this variability reaches statistical significance only for geographic area of the study. In formal meta-regression, however, none of these study characteristics are significant study-level covariates accounting for the heterogeneity of HPV prevalence. Finally, it is important to note that this study does not analyze the physical state or transcriptional activity of HPV in these tumors. Multicentric follow-up studies are needed to further characterize the role of HPV in LSCC.

CONCLUSION

In stratified meta-analysis, variability in HPV detection rates in LSCC is explained by geographic area of the studies and not by HPV detection method. None of the two were significant study-level covariates in formal meta-regression.

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